

#3  
0420  
03CO

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/054,680

DATE: 02/12/2002

TIME: 12:08:02

Input Set : A:\LEX-0301-USA SEQLIST.txt

Output Set: N:\CRF3\02122002\J054680.raw

**ENTERED**

4 <110> APPLICANT: Friddle, Carl Johan  
 5 Hilbun, Erin  
 7 <120> TITLE OF INVENTION: Novel Human Ion Exchanger Proteins and Polynucleotides

Encoding the  
 8 Same

10 <130> FILE REFERENCE: LEX-0301-USA  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/054,680  
 C--> 12 <141> CURRENT FILING DATE: 2002-01-22  
 12 <150> PRIOR APPLICATION NUMBER: US 60/263,384  
 13 <151> PRIOR FILING DATE: 2001-01-23  
 15 <160> NUMBER OF SEQ ID NOS: 5  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2766  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: homo sapiens  
 24 <400> SEQUENCE: 1

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 26 tttgtgctct tcctgaatgg tcttcgagca gaggtctggt gctcagggga cgtgccaaagc 120  
 27 acagggcaga acaatgagtc ctgttcaggg tcatcggaact gcaaggaggg tgtcatcctg 180  
 28 ccaatctggt acccgagaa cccttccctt ggggacaaga ttgccagggt cattgtctat 240  
 29 tttgtggccc tgatatacat gttccttggt gtgtccatca ttgctgaccg cttcatggca 300  
 30 tctattgaag tcatcacctc tcaagagagg gaggtgacaa ttaagaaacc caatggagaa 360  
 31 accagcacia ccactattcg ggtctggaat gaaactgtct ccaacctgac ccttatggcc 420  
 32 ctgggttctt ctgctcctga gatactcttc tctttaattg aggtgtgtgg tcatgggttc 480  
 33 attgctggtg atctgggacc ttctaccatt gtagggagtg cagccttcaa catgttcatt 540  
 34 atcattggca tctgtgtcta cgtgatccca gacggagaga ctgcgaagat caagcatcta 600  
 35 cgagtcttct tcatcacccg tgcttgaggt atctttgcct acatctggtt ctatatgatt 660  
 36 ctggcagctt tctcccttgg tgtgtccag gtttgggaag gcctcctcac tctcttcttc 720  
 37 tttccagtgt gttccttctt ggcctgggtg gcagataaac gactgctctt ctacaaatac 780  
 38 atgcacaaaa agtaccgcac agacaaacac cgaggaatta tcatagagac agagggtgac 840  
 39 caccctaagg gcattgagat ggatgggaaa atgatgaatt cccattttct agatgggaac 900  
 40 ctgggtcccc tggaaggga ggaagtggat gactcccgca gagagatgat ccggattctc 960  
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 42 tactatgtct tttcccacca acagaagagc cgcgccttct accgtatcca agccactcgt 1080  
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 50 gcaatattca acagtcttcc cttgcctcgg gctgtcctag cctccccttg tgtggccaca 1560  
 51 gttaccatct tggatgatga ccatgcaggc atcttcactt ttgaatgtga tactattcat 1620

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52 gtcagtgaga gtattggtgt tatggaggtc aagggttctgc ggacatcagg tgccccggggt 1680
53 acagtcatcg tccccttttag gacagtagaa gggacagcca aggggtggcgg tgaggacttt 1740
54 gaagacacat atggggaggtt ggaattcaag aatgatgaaa ctgtgaaaac cataagggtt 1800
55 aaaaatagtag atgaggagga atacgaaagg caagagaatt tcttcattgc ccttggtgaa 1860
56 ccgaaatgga tggaacgtgg aatatcagat gtgacagaca ggaagctgac tatggaagaa 1920
57 gaggaggcca agaggatagc agagatggga aagccagtat tgggtgaaca ccccaaacta 1980
58 gaagtcacatc ttgaagagtc ctatgagttc aagactacgg tggacaaact gatcaagaag 2040
59 acaaacctgg ccttggttgt ggggacccat tcctggaggg accagttcat ggaggccatc 2100
60 accgtcagtg cagcagggga tgaggatgag gatgaatccg gggaggagag gctgcctcc 2160
61 tgctttgact acgtcatgca ctctctgact gtcttctgga aggtgctgtt tgctgtgtg 2220
62 cccccacag agtactgcca cggttgggccc tgcttcgccc tctccatcct catcattggc 2280
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69 ctgggagggg agcttggtgg ccccgtggc tgcaagctcg ccacaacatg gctctttgtg 2700
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73 &lt;210&gt; SEQ ID NO: 2

74 &lt;211&gt; LENGTH: 921

75 &lt;212&gt; TYPE: PRT

76 &lt;213&gt; ORGANISM: homo sapiens

78 &lt;400&gt; SEQUENCE: 2

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81 Gly Leu Val Thr Phe Val Leu Phe Leu Asn Gly Leu Arg Ala Glu Ala
82 20 25 30
83 Gly Gly Ser Gly Asp Val Pro Ser Thr Gly Gln Asn Asn Glu Ser Cys
84 35 40 45
85 Ser Gly Ser Ser Asp Cys Lys Glu Gly Val Ile Leu Pro Ile Trp Tyr
86 50 55 60
87 Pro Glu Asn Pro Ser Leu Gly Asp Lys Ile Ala Arg Val Ile Val Tyr
88 65 70 75 80
89 Phe Val Ala Leu Ile Tyr Met Phe Leu Gly Val Ser Ile Ile Ala Asp
90 85 90 95
91 Arg Phe Met Ala Ser Ile Glu Val Ile Thr Ser Gln Glu Arg Glu Val
92 100 105 110
93 Thr Ile Lys Lys Pro Asn Gly Glu Thr Ser Thr Thr Thr Ile Arg Val
94 115 120 125
95 Trp Asn Glu Thr Val Ser Asn Leu Thr Leu Met Ala Leu Gly Ser Ser
96 130 135 140
97 Ala Pro Glu Ile Leu Leu Ser Leu Ile Glu Val Cys Gly His Gly Phe
98 145 150 155 160
99 Ile Ala Gly Asp Leu Gly Pro Ser Thr Ile Val Gly Ser Ala Ala Phe
100 165 170 175
101 Asn Met Phe Ile Ile Ile Gly Ile Cys Val Tyr Val Ile Pro Asp Gly
102 180 185 190

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103 Glu Thr Arg Lys Ile Lys His Leu Arg Val Phe Phe Ile Thr Ala Ala
104          195          200          205
105 Trp Ser Ile Phe Ala Tyr Ile Trp Leu Tyr Met Ile Leu Ala Val Phe
106      210          215          220
107 Ser Pro Gly Val Val Gln Val Trp Glu Gly Leu Leu Thr Leu Phe Phe
108 225          230          235          240
109 Phe Pro Val Cys Val Leu Leu Ala Trp Val Ala Asp Lys Arg Leu Leu
110          245          250          255
111 Phe Tyr Lys Tyr Met His Lys Lys Tyr Arg Thr Asp Lys His Arg Gly
112          260          265          270
113 Ile Ile Ile Glu Thr Glu Gly Asp His Pro Lys Gly Ile Glu Met Asp
114      275          280          285
115 Gly Lys Lys Met Met Asn Ser His Phe Leu Asp Gly Asn Leu Val Pro Leu
116      290          295          300
117 Glu Gly Lys Glu Val Asp Glu Ser Arg Arg Glu Met Ile Arg Ile Leu
118 305          310          315          320
119 Lys Asp Leu Lys Gln Lys His Pro Glu Lys Asp Leu Asp Gln Leu Val
120          325          330          335
121 Glu Met Ala Asn Tyr Tyr Ala Leu Ser His Gln Gln Lys Ser Arg Ala
122          340          345          350
123 Phe Tyr Arg Ile Gln Ala Thr Arg Met Met Thr Gly Ala Gly Asn Ile
124      355          360          365
125 Leu Lys Lys His Ala Ala Glu Gln Ala Lys Lys Ala Ser Ser Met Ser
126      370          375          380
127 Glu Val His Thr Asp Glu Pro Glu Asp Phe Ile Ser Lys Val Phe Phe
128 385          390          395          400
129 Asp Pro Cys Ser Tyr Gln Cys Leu Glu Asn Cys Gly Ala Val Leu Leu
130          405          410          415
131 Thr Val Val Arg Lys Gly Gly Asp Met Ser Lys Thr Met Tyr Val Asp
132          420          425          430
133 Tyr Lys Thr Glu Asp Gly Ser Ala Asn Ala Gly Ala Asp Tyr Glu Phe
134      435          440          445
135 Thr Glu Gly Thr Val Val Leu Lys Pro Gly Glu Thr Gln Lys Glu Phe
136      450          455          460
137 Ser Val Gly Ile Ile Asp Asp Asp Ile Phe Glu Glu Asp Glu His Phe
138 465          470          475          480
139 Phe Val Arg Leu Ser Asn Val Arg Ile Glu Glu Glu Gln Pro Glu Glu
140          485          490          495
141 Gly Met Pro Pro Ala Ile Phe Asn Ser Leu Pro Leu Pro Arg Ala Val
142          500          505          510
143 Leu Ala Ser Pro Cys Val Ala Thr Val Thr Ile Leu Asp Asp Asp His
144      515          520          525
145 Ala Gly Ile Phe Thr Phe Glu Cys Asp Thr Ile His Val Ser Glu Ser
146      530          535          540
147 Ile Gly Val Met Glu Val Lys Val Leu Arg Thr Ser Gly Ala Arg Gly
148 545          550          555          560
149 Thr Val Ile Val Pro Phe Arg Thr Val Glu Gly Thr Ala Lys Gly Gly
150          565          570          575
151 Gly Glu Asp Phe Glu Asp Thr Tyr Gly Glu Leu Glu Phe Lys Asn Asp

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152          580          585          590
153 Glu Thr Val Lys Thr Ile Arg Val Lys Ile Val Asp Glu Glu Glu Tyr
154          595          600          605
155 Glu Arg Gln Glu Asn Phe Phe Ile Ala Leu Gly Glu Pro Lys Trp Met
156          610          615          620
157 Glu Arg Gly Ile Ser Asp Val Thr Asp Arg Lys Leu Thr Met Glu Glu
158 625          630          635          640
159 Glu Glu Ala Lys Arg Ile Ala Glu Met Gly Lys Pro Val Leu Gly Glu
160          645          650          655
161 His Pro Lys Leu Glu Val Ile Ile Glu Glu Ser Tyr Glu Phe Lys Thr
162          660          665          670
163 Thr Val Asp Lys Leu Ile Lys Lys Thr Asn Leu Ala Leu Val Val Gly
164          675          680          685
165 Thr His Ser Trp Arg Asp Gln Phe Met Glu Ala Ile Thr Val Ser Ala
166          690          695          700
167 Ala Gly Asp Glu Asp Glu Asp Glu Ser Gly Glu Glu Arg Leu Pro Ser
168 705          710          715          720
169 Cys Phe Asp Tyr Val Met His Phe Leu Thr Val Phe Trp Lys Val Leu
170          725          730          735
171 Phe Ala Cys Val Pro Pro Thr Glu Tyr Cys His Gly Trp Ala Cys Phe
172          740          745          750
173 Ala Val Ser Ile Leu Ile Ile Gly Met Leu Thr Ala Ile Ile Gly Asp
174          755          760          765
175 Leu Ala Ser His Phe Gly Cys Thr Ile Gly Leu Lys Asp Ser Val Thr
176          770          775          780
177 Ala Val Val Phe Val Ala Phe Gly Thr Ser Val Pro Asp Thr Phe Ala
178 785          790          795          800
179 Ser Lys Ala Ala Ala Leu Gln Asp Val Tyr Ala Asp Ala Ser Ile Gly
180          805          810          815
181 Asn Val Thr Gly Ser Asn Ala Val Asn Val Phe Leu Gly Ile Gly Leu
182          820          825          830
183 Ala Trp Ser Val Ala Ala Ile Tyr Trp Ala Leu Gln Gly Gln Glu Phe
184          835          840          845
185 His Val Ser Ala Gly Thr Leu Ala Phe Ser Val Thr Leu Phe Thr Ile
186          850          855          860
187 Phe Ala Phe Val Cys Ile Ser Val Leu Leu Tyr Arg Arg Arg Pro His
188 865          870          875          880
189 Leu Gly Gly Glu Leu Gly Gly Pro Arg Gly Cys Lys Leu Ala Thr Thr
190          885          890          895
191 Trp Leu Phe Val Ser Leu Trp Leu Leu Tyr Ile Leu Phe Ala Thr Leu
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193 Glu Ala Tyr Cys Tyr Ile Lys Gly Phe
194          915          920
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1863
199 <212> TYPE: DNA
200 <213> ORGANISM: homo sapiens
202 <400> SEQUENCE: 3
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DATE: 02/12/2002

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Input Set : A:\LEX-0301-USA SEQLIST.txt

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204 tttgtgctct tctgaatgg tcttcgagca gaggctggtg gctcagggga cgtgccaaagc 120
205 acagggcaga acaatgagtc ctgttcaggg tcatcgact gcaaggaggg tgtcatcctg 180
206 ccaatctggt acccgagaa cccttccctt ggggacaaga ttgccagggg cattgtctat 240
207 tttgtggccc tgatatacat gttccttggg gtgtccatca ttgctgaccg cttcatggca 300
208 tctattgaag tcatcacctc tcaagagagg gaggtagaaa ttaagaaacc caatggagaa 360
209 accagcacia ccactattcg ggtctggaat gaaactgtct ccaacctgac cttatggcc 420
210 ctgggttccct ctgctcctga gatactcctc tctttaattg aggtgtgtgg tcatgggttc 480
211 attgctggtg atctgggacc ttctaccatt gtagggagtg cagccttcaa catgttcac 540
212 atcattggca tctgtgtcta cgtgatccca gacggagaga ctgcaagat caagcatcta 600
213 cgagtcttct tcatcaccgc tgcctggagt atctttgcct acatctggct ctatatgatt 660
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227 tttgtaagggt tgagcaatgt ccgcatagag gaggagcagc cagaggaggg gatgcctcca 1500
228 gcaatattca acagtcttcc cttgcctcgg gctgtcctag cctccccttg tgtggccaca 1560
229 gttaccatct tggatgatga ccatgcaggc atcttcaact ttgaatgtga tactattcat 1620
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231 acagtcatcg tcccctttag gacagtagaa gggacagcca aggggtggcg tgaggacttt 1740
232 gaagacacat atggggagtt ggaattcaag aatgatgaaa ctgtatgtga cagacaggaa 1800
233 gctgactatg gaagaagagg aggccaaagag gatagcagag atgggaaagc cagtattggg 1860
234 tga

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236 &lt;210&gt; SEQ ID NO: 4

237 &lt;211&gt; LENGTH: 620

238 &lt;212&gt; TYPE: PRT

239 &lt;213&gt; ORGANISM: homo sapiens

241 &lt;400&gt; SEQUENCE: 4

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245 20 25 30
246 Gly Gly Ser Gly Asp Val Pro Ser Thr Gly Gln Asn Asn Glu Ser Cys
247 35 40 45
248 Ser Gly Ser Ser Asp Cys Lys Glu Gly Val Ile Leu Pro Ile Trp Tyr
249 50 55 60
250 Pro Glu Asn Pro Ser Leu Gly Asp Lys Ile Ala Arg Val Ile Val Tyr
251 65 70 75 80
252 Phe Val Ala Leu Ile Tyr Met Phe Leu Gly Val Ser Ile Ile Ala Asp
253 85 90 95
254 Arg Phe Met Ala Ser Ile Glu Val Ile Thr Ser Gln Glu Arg Glu Val

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VERIFICATION SUMMARY

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DATE: 02/12/2002

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Input Set : A:\LEX-0301-USA SEQLIST.txt

Output Set: N:\CRF3\02122002\J054680.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date